GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:57:52 ; Search time 31.07 Seconds
                       (without alignments)
                       3253.332 Million cell updates/sec

Title: US-09-587-111-5
Perfect score: 4004
Sequence: 1 MTSPSSSPVFRLETLDGGQE............EDEDGASEENVPVQOLLQSN 764

Scoring table: BLOSUM62
                       Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 133205027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : SPTREMBL_16:*
     1: sp_archea:*
     2: sp_bacteria:*
     3: sp_fungi:*
     4: sp_human:*
     5: sp_invertebrate:*
     6: sp_mammal:*
     7: sp_mhc:*
     8: sp_organelle:*
     9: sp_phage:*
    10: sp_plant:*
    11: sp_rodent:*
    12: sp_unclassified:*
    13: sp_vertebrate:*
    14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	4004	100.0	764	4	Q9Y5S1	Q9y5s1 homo sapien
2	3945	98.5	764	4	Q9Y670	Q9y670 homo sapien
3	3159	78.9	756	11	Q9WTR1	Q9wtr1 mus musculu
4	3051.5	76.2	761	11	Q9WUD2	Q9wud2 rattus norv
5	3041.5	76.0	761	11	Q9QYH8	Q9qyh8 rattus norv
6	3028.5	75.6	762	11	Q9JMI8	Q9jmi8 rattus norv
7	1652	41.3	838	11	O35433	O35433 rattus norv
8	1652	41.3	838	11	Q9JM57	Q9jm57 rattus norv
9	1651.5	41.2	839	4	Q9H304	Q9h304 homo sapien
10	1648.5	41.2	839	4	Q9H0G9	Q9h0g9 homo sapien
11	1644.5	41.1	839	4	Q9NQ74	Q9nq74 homo sapien
12	1636.5	40.9	839	4	Q9NY22	Q9ny22 homo sapien
13	1467	36.6	852	13	Q9DFS3	Q9dfs3 gallus gall
14	1467	36.6	871	4	Q9HBC0	Q9hbc0 homo sapien
15	1465.5	36.6	871	11	Q9ER28	Q9er28 rattus norv
16	1464	36.6	871	4	Q9HBA0	Q9hba0 homo sapien
17	1458.5	36.4	871	11	Q9ES76	Q9es76 mus musculu
18	1457.5	36.4	871	11	Q9EPK8	Q9epk8 mus musculu
19	1452.5	36.3	871	11	Q9EQ24	Q9eq24 mus musculu
20	1446.5	36.1	873	11	Q9ERZ7	Q9erz7 mus musculu
21	1442.5	36.0	778	11	Q9JM56	Q9jm56 rattus norv
22	1112.5	27.8	528	11	Q92182	Q92182 rattus norv
23	969	24.2	511	4	Q9H303	Q9h303 homo sapien
24	933	23.3	471	11	Q9LM0	Q9lm0 rattus norv
25	634	15.8	725	4	Q9H296	Q9h296 homo sapien
26	631	15.8	725	4	Q9H1D1	Q9h1d1 homo sapien
27	630	15.7	725	4	Q9H1D0	Q9h1d0 homo sapien
28	607.5	15.2	727	11	Q9R186	Q9r186 rattus norv
29	589	14.7	723	11	Q9JIP0	Q9jip0 rattus norv
30	586	14.6	730	6	Q9XSM3	Q9xsm3 oryctolagus
31	584	14.6	723	11	Q9JIL2	Q9jil2 rattus norv
32	579.5	14.5	729	4	Q9NQA5	Q9nqa5 homo sapien
33	469.5	11.7	769	11	Q9N3Y9	Q9n3y9 caenorhabdi
34	440.5	11.0	729	11	Q9JJJ0	Q9jjj0 mus musculu
35	428.5	10.7	750	5	Q9VUD5	Q9vud5 drosophila
36	414	10.3	750	5	Q61220	Q61220 caenorhabdi
37	392.5	9.8	900	5	Q22374	Q22374 caenorhabdi
38	364	9.1	937	5	Q9W3W0	Q9w3w0 drosophila
39	338	8.4	790	5	O17469	O17469 caenorhabdi
40	261	6.5	1123	5	Q9VUD5	Q9vud5 drosophila
41	255	6.4	519	5	Q22374	Q22374 caenorhabdi
42	233	5.8	1913	5	Q9GRV5	Q9grv5 caenorhabdi
43	229	5.7	904	5	Q9W0T5	Q9w0t5 drosophila
44	226.5	5.7	1453	5	Q9VMR4	Q9vmr4 drosophila
45	224.5	5.6	981	6	P79100	P79100 bos taurus
			890	11	Q9QUQ9	Q9quq9 mus musculu

ALIGNMENTS

RESULT   1

ID   Q9Y5S1   PRELIMINARY;   PRT;   764 AA.
AC   Q9Y5S1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN   VRL-1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99215558; PubMed=10201375;
RA   Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT   "A capsaicin-receptor homologue with a high threshold for noxious
RT   heat.";
RL   Nature 398:436-441(1999).
DR   EMBL; AF129112; AAD26363.1; -.
DR   InterPro; IPR002110; -.
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS00088; ANK_REPEAT; 1.
DR   PROSITE; PS50088; ANK_REP_REGION; 1.
DR   PROSITE; PS50297; ANK; 1.
DR   SMART; SM00248; ANK; 1.
KW   Receptor.
SQ   SEQUENCE   764 AA; 85980 MW; A73E3696E70F91E9 CRC64;

Query Match   100.0%; Score 4004; DB 4; Length 764;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MTSPSSSPVFRLETLDGGQEDGSEADRGKLDFGSGLPPMESQFOGEDRKFAPQIRVNLNY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MTSPSSSPVFRLETLDGGQEDGSEADRGKLDFGSGLPPMESQFOGEDRKFAPQIRVNLNY 60

Qy   61 RKGTGASQPDNRFRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTTCL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RKGTGASQPDNRFRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTTCL 120

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Qy   121  MKAVLNLIKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  MKAVLNLIKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK  180

Qy   181  LIVENGANVHARACGRFFQKQGGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  LIVENGANVHARACGRFFQKQGGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA   240

Qy   241  TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL   300

Qy   301  AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF   360

Qy   361  HCKSPHRHRMVVLEPLNKLLQAKWDLLIPKFLNFLCNLIYMFIFTAVAYHQPTLKKQAA   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  HCKSPHRHRMVVLEPLNKLLQAKWDLLIPKFLNFLCNLIYMFIFTAVAYHQPTLKKQAA   420

Qy   421  PHLKAEVGNSMLLTGHIILILGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALL   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  PHLKAEVGNSMLLTGHIILILGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALL   480

Qy   481  TVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLL   540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLL   540

Qy   541  IYLVLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLEL   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  IYLVLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLEL   600

Qy   601  FKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIW   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  FKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIW   660

Qy   661  KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPT   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPT   720

Qy   721  LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
          ||||||||||||||||||||||||||||||||||||||||||||
Db   721  LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
```

```
RESULT 2
ID   Q9Y670              PRELIMINARY;   PRT;   764 AA.
AC   Q9Y670;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR-LIKE PROTEIN.
GN   VRL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Garcia R.L., Delmas P., England S., Liapi A., Wood J.N.;
RT   "Cloning and functional expression of VRL, a vanilloid receptor-like
RT   gene.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF103906; AAD41724.1; -.
DR   InterPro; IPR002110; -.
DR   InterPro; IPR002111; -.
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   SMART; SM00248; ANK; 1.
KW   Receptor.
```

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SQ   SEQUENCE   764 AA;  86053 MW;  AF9DE88F495EB443A0 CRC64;

Query Match             98.5%;           Score 3945;   DB 4;   Length 764;
Best Local Similarity   98.2%;           Pred. No. 0;
Matches  750;  Conservative   6;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  MTSPSSSPVFRLETLDGGQEDGSEADRGKLDFGSGLPPMESQFQGGEDRKFAPQIRVNLNY   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    1  MTSPSSSPVFRLETLDGGQEDGSEADRGKLDFGSGLPPMESQFQGGEDRKFASQIRVNLNY   60

Qy   61  RKGTGASQPDPNRFDRDRLFNAVSRGVPEDLAGILPEYLSKTSKRYLTDSEYTEGSTGKTCL  120
         ||||||||||||   |||||   |||||||  | ||||||||| ||||| ||||||| |||
Db   61  RKGTGASQPDPNRFRDRDRLFNVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL   120

Qy  121  MKAVLNLIKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  MKAVLNLIKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK  180

Qy  181  LIVENGANVHARACGRFFQKQGGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA   240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  LIVENGANVHARACGRFFQKQGGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA   240

Qy  241  TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL   300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL   300

Qy  301  AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF   360

Qy  361  HCKSPHRHRMVVLEPLNKLLQAKWDLLIPKFLNFLCNLIYMFIFTAVAYHQPTLKKQAA   420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  HCKSPHRHRMVVLEPLNKLLQAKWDLLIPKFLNFLCNLIYMFIFTAVAYHQPTLKKQAA   420

Qy  421  PHLKAEVGNSMLLTGHIILILGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALL   480
         ||||||||||||||||||||||||||||||||||||||||||  | ||||||||||
Db  421  PHLKAEVGNSMLLTGHIILILGGIYLLVGQLWYFWRRHVFIWISYTDSYFEILFHSLL   480

Qy  481  TVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLL   540
         |||||||  ||  |||||||||||||||||||||||||||||||||||||||||: :||::
Db  481  TVVSQVLCFLVIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDMVRFLV   540

Qy  541  IYLVLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLEL   600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  IYLVLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLEL   600

Qy  601  FKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIW   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  FKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIW   660

Qy  661  KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPT   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPT   720

Qy  721  LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
         ||||||||||||||||||||||||||||||||||||||||||||
Db  721  LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
```

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RESULT 3
ID   Q9WTR1              PRELIMINARY;   PRT;   756 AA.
AC   Q9WTR1;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   GROWTH FACTOR REGULATED CALCIUM CHANNEL.
GN   VRL1 OR GRC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

```
Qy  601  FKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIW   660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  FKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSIW   660

Qy  661  KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPT   720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTLPT   720

Qy  721  LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
         |||||||||||||||||||||||||||||||||||||||||||
Db  721  LCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57 BLACK-6; TISSUE=SPLEEN;
RA   Kanzaki M., Zhang Y., Kojima I.;
RL   "Growth factor regulated calcium channel.";
RT   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB021665; BAA78478.1; -.
DR   MGD; MGI:1341836; Vrl1.
DR   InterPro; IPR002110; -.
DR   InterPro; IPR002111; -.
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   SMART; SM00248; ANK; 1.
SQ   SEQUENCE   756 AA;   85964 MW;   4C037D0F6066EF4C CRC64;

Query Match             78.9%;  Score 3159;  DB 11;  Length 756;
Best Local Similarity   80.3%;  Pred. No. 7.2e-241;
Matches   615;  Conservative   55;  Mismatches   84;  Indels   12;  Gaps   5;

Qy    1  MTSPSSPVFRLEETLDGGQEDGSEADRGKLDFGSGLPPMESQFQCGEDRKFAPQIRVNLNY   60
            ||||:||| |||||| ||||||||||:||||||:|||||||||  :|:|||||||||||
Db    1  MTSASNPPAFRLETSDGDEEGSAEVNKGK----NEPPPMESPFQQEDRNFSPQIRVNLNY   56

Qy   61  RKGTGASQDPDNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL  120
         |:|  ||||||||||||||:||  :|:||||||:|||||||||||||||||||||||||||
Db   57  RKGLGPSQQDPDNRFDRDRLFSVVSRGVPEELTGLLEYLRRTSKYLTDSAYTEGSTGKTCL  116

Qy  121  MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK  180
         |||||||:|||||||||||||| |||||||||||||||| :|||||||||||||||| |||
Db  117  MKAVLNLQDGVNACILPLLQIDIRDRSGNPQPLVNAQCTDDEFYRGHSALHIAIEKRSLWCVK  176

Qy  181  LIVENGANVHARACGRFFQKQGQTGCFYFGELPLSLAACTKQWDVSYLLENPHQPASLQA  240
         ||||||||| :|||||||||  | :||:||||||||||||||||| :|||||||||||:|
Db  177  LIVENGANVHIRACGRFFQKHQGTCYFGELPLSLAACTKQWDVVTYLLENPHQPASLEA  236

Qy  241  TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL  300
         |||.|||||||||||:||||:||:||:|||:|||:|||||||||||||:.|:|.||||||
Db  237  TDSLGNTVLHALVMIADNSPENSALVIHMYDSLLQMGARLCPTVQLEDICNHQGLTPLKL  296

Qy  301  AAKEGKIEIFRHILQREFSGL-SHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIA  359
         |||||||||||||||||||||  |||||||||||||||||||||:|||| .|||||||||
Db  297  AAKEGKIEIFRHILQREFSGLYQPLSRKFTEWCYGPVRVSLYDLSSVDSWEKNSVLEIIA  356

Qy  360  FHCKSPHRHRMVVLEPLNKLLQAKWDLLIPKFFLNEFLCNLIYMFIFTAVAYHQPTLKQA  419
         ||||||||||||||||||||||  :||.|||:||:||.|:|||||||| |:.|||||:|
Db  357  FHCKSPHRHRMVVLEPLNKLLQEKWDRLIPRFFNFACYLVYMFIFTIVVAYHQPSLEQPA  416

Qy  420  APHLKAEVGNSMLLTGHILILILGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQAL  479
          | .||| |:|||| |||||| ||||||| ||||||||| :|||||| :|||||||| |||
Db  417  IPSSKATFGDSMLLLGHILILLGGIYLLLGQLWYFWRRRLFIWISFMDSYFEILFLVQAL  476

Qy  480  LTVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLRFL  539
         |||.||||.|:. |||||||||:||||||||||||||||||||||||||||||||| |||
Db  477  LTVLSQVLRFVETEWYLPLLVSSLVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFL  536

Qy  540  LIILVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGGQEDEGNGAQYRGILEASLE  599
         |.||||||||||||||||.||   .||.|   : : |:|  .|:|.|||   |||.|||
Db  537  LVILVFLFGFAVALVSLSREARSKPAPENSNTIVTEKPILGQEEE--PVPYGGILDASLE  594

Qy  600  LFKFTIGMGELAFQEOLHFRGMVLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSI  659
         |||||||||||||||||:|||:||||||||||||:||||||||||||| |||||||||||
Db  595  LFKFTIGMGELAFQEOLRFRGVVLLLLAYVLLTYVLLLNMLIALMSEIVNSVATDSWSI  654

Qy  660  WKLQKAISVLEMENGYWCRKKQ-RAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTL  718
         ||||||||||||||||| ||:  :|||.|| |||.||.|||||||||||||||:||:.||
Db  655  WKLQKAISVLEMENGYWWCRKRKIHRAGRLLKVGTKGDGIPDERWCFRVEEVNWAAWEKTL  714

Qy  719  PTLCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN  764
         |||.|||||||: |||        :|.|.|||||  || :|.|||.|
Db  715  PTLSEDPSGAGIIGYKKNPT----SKPGKNSASEEDHLPLQVLQSH  756
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RESULT   4
ID   Q9WUD2       PRELIMINARY;   PRT;   761 AA.
AC   Q9WUD2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR-LIKE PROTEIN 1.
GN   VRL-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=99215558; PubMed=10201375;
RA   Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT   "A capsaicin-receptor homologue with a high threshold for noxious
RT   heat.";
RL   Nature 398:436-441(1999).
DR   EMBL; AF129113; AAD26364.1; -.
DR   InterPro; IPR002110; -.
DR   InterPro; IPR002111; -.
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   SMART; SM00248; ANK; 1.
KW   Receptor.
SQ   SEQUENCE   761 AA;   86689 MW;   46A281183EB6672F CRC64;

Query Match             76.2%;  Score 3051.5;  DB 11;  Length 761;
Best Local Similarity   77.8%;  Pred. No. 2.2e-232;
Matches   598;  Conservative   62;  Mismatches   93;  Indels   17;  Gaps   7;

Qy    1  MTSPSSPVFRLEETLDGGQEDGSEADRGKLDFGSGLPPMESQFQCGEDRKFAPQIRVNLNY   60
            |||||| ||||:|||||||:|||.|||::|||    |||||||:|:|||.||||||||||:
Db    1  MTSASSPPAFRLETSDGDEEGNAEVNNGKQE----PPPMESPFQREDRNSSPQIRVNLNF   56

Qy   61  ----RKGTGA-SQPDPNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGST  115
              ||| ||: ||.:|.|||||||||:||:|||||||:|||||:|||||||||||||||||
Db   57  IKRPPKNTSAPSQQEPDRFDRDRLFSVVSRGVPEELTGLLEYLRWNSKYLTDSAYTEGST  116

Qy  116  GKTCLMKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRS  175
         |||||||||||:|||||||:.||||||:|||||:|||||||||| :||.||||||||||||
Db  117  GKTCLMKAVLNLQDGVNACIMPLLQIDKDSGNPKPLVNAQCTDDEFYGGHSALHIAIEKRS  176

Qy  176  LQCVKLLVENGANVHARACGRFFQKQGQTGCFYFGELPLSLAACTKQWDVSYLLENPHQP  235
         |||||||||||| ||:||||||||||  | :||:|||||||||||||||||| ||||||||
Db  177  LQCVKLLVENGADVHLRACGRFFQKHQGTCYFGELPLSLAACTKQWDVVTYLLENPHQP  236

Qy  236  ASLQATDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDL  295
         ||| ||||.|||||||||||:||||:||:||:||||||||:||||||||||||:|:||:|
Db  237  ASLEATDSLGNTVLHALVMIADNSPENSALVIHMYDGLLQMGARLCPTVQLEDEISNHQGL  296

Qy  296  TPLKLAAKEGKIEIFRHILQREFSG-LSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSV  354
         |||||||||||||||||||||||||  ||||||||||||||||||||||:|||| .||||
Db  297  TPLKLAAKEGKIEIFRHILQREFSGPYQPLSRKFTEWCYGPVRVSLYDLSSVDSWEKNSV  356

Qy  355  LEIIAFHCKSPHRHRMVVLEPLNKLLQAKWDLLIPKFFLNEFLCNLIYMFIFTAVAYHQPT  414
         |||||||||||:||||||||||||||||  :||.|.:||:||.|:||||||||| |:.|||:
Db  357  LEIIAFHCKSPNRHRMVVLEPLNKLLQEKWDRLVSRFFNFACYLVYMFIFTIVVAYHQPS  416

Qy  415  LKKQAAPHLKAEVGNSMLLTGHILILILGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILF  474
         |..:| | .||| |:|||| |||||| ||||||| ||||||||| :|||||| :|||||||
Db  417  LDQPAIPSSKATFGESMLLLGHILILLGGIYLLLGQLWYFWRRRLFIWISFMDSYFEILF  476

Qy  475  LFQALLTVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRD  534
         | ||||||.||||.|:. |||||||| :||||||||||||||||||||||||||||||||
Db  477  LLQALLTVLSQVLRFMETEWYLPLLVLSLVLGWLNLLYYTRGFQHTGIYSVMIQKVILRD  536
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Qy    535  LIRFLLIYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGGQEDEGNGAQYRGIL 594
           :||:||||||:||||||:||||||| ||   |:: || |||  ||| | |||
Db    537  LLRFLLVYLIVFLFGFAVALVSLSREARSPKAPEDNNSTVTEQPTVGQEE--PAPYRSIL 594

Qy    595  EASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLITYILLLNMLILMSETVNSVAT 654
           :  ||||||||||||||||||||||| |:||||||||||||||||||||||| |||||
Db    595  DASLELFKFTIGMGELAFQEQLRFRGVVLLLLLAYVLLITYVLLLNMLIALMSETVNHVAD 654

Qy    655  DSWSIWKLQKAISVLEMENGYWWC-RKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNNAS 713
           :||||||||:|||||||||||||| |||||||||||||||||||||||||||||||:|
Db    655  NSWSIWKLQKAISVLEMENGYWWCRKKRKHREGRLLKVGTRGDGTPDERWCFRVEEVNNAA 714

Qy    714  WEQTLPTLCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQS 763
           ||:||||||||||||||||||||||||||||  :||||::|:|:|:|||
Db    715  WEKTLPTLSEDPSGPGITGNKKNPT----SKPGKNSASEEDHLPLQVLQS 760
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RESULT  5
ID    Q90YH8           PRELIMINARY;         PRT;     761 AA.
AC    Q90YH8;
DT    01-MAY-2000 (TrEMBLrel. 13, Created)
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE    STRETCH ACTIVATED CHANNEL 2B.
GN    RSAC2B.
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX    NCBI_TaxID=10116;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Ishibashi K.;
RL    "Molecular cloning of a stretch activated channel from rat kidney.";
RL    Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AB029330; BAA88637.1; -.
DR    InterPro; IPR002110; -.
DR    InterPro; IPR002111; -.
DR    Pfam; PF00023; ank; 3.
DR    PROSITE; PS50088; ANK_REPEAT; 1.
DR    PROSITE; PS50297; ANK_REP_REGION; 1.
DR    PROSITE; PS50297; ANK_REP_REGION; 1.
SM    SMART; SM00248; ANK; 1.
SQ    SEQUENCE   761 AA;  86705 MW;  8977CDE1D5351EC8 CRC64;
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Query Match             76.0%;  Score 3041.5;  DB 11;  Length 761;
Best Local Similarity   77.5%;  Pred. No. 1.4e-231;
Matches  597;  Conservative  62;  Mismatches  94;  Indels  17;  Gaps  7;
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Qy      1  MTSPSPSSSPVFRLETLDGQOEDGSEADRGKLDFGSGLPPMESOFQGEDRKFAPQIRVNLNY 60
           |||:||| ||:| || | :|   :|||||| ||| ||||||:||:::||||| :|||||:
Db      1  MTSASSPPAFRLETSDGDEEGNAEVNKGKQE----PPPMESPFQREDRNSSPQIKVNLNF 56

Qy     61  ----RKGTGA-SOQPDNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGST 115
           |||| | || :|:|||:|||| ||:|:|||||:|||:||||||||||||||||||||||
Db     57  IKRPPKNTSAPSQOEPDRFDRDRLFSVVSRGVPEELTGLLEYLRWNSKYLTDSAYTEGST 116

Qy    116  GKTCLMKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGHSALHIAIEKRS 175
           |||||||||||||||||||||:||||||||||||||||||||||:|||||||||||||
Db    117  GKTCLMKAVLNLQODGVNACIMPLLQIDKDSGNPKLLVNAQCTDEFYQGHSALHIAIEKRS 176

Qy    176  LQCVKLLVENGANVHARACGRFFQKQGCGTCYFGEPLPLSLAACTKQWDVSYLLENPHQP 235
           ||||||||||||||||:||||| :||:|:||:|| |||||| |:|||||||||||:||||
Db    177  LQCVKLLVENGADVHLRACGRFFQKHQGTCTFYFGELPLSLAACTKQWDVVTLLENPHQP 236

Qy    236  ASLQATDSQGNTIVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDL 295
           ||| ||||:||||||||||||| |||||| ||:|||||||||:|| |||||||:||||:|
Db    237  ASLEATDSLGNTVLHALVMIADNSPENSALVTHMYDGLLQMGARLCPTVQLEEISNHQGL 296

Qy    296  TPLKLAAKEGKIEIFRHILQREFSG--LSHLSRKFTEWCYGPVRVSLYLDFLASVDSCEENSV 354
           |||||||||:|||||||:|||||||  | :|||||||||||:|||| |||| ||||:|||||
Db    297  TPLKLAAKEGKIEIFRHILQREFSGPYQPLSRKFTEWCYGPVRVSLYLDLSSVDSWEKNSV 356
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Qy    355  LEIIAFHCKSPHRHRMVVLEPLKNLLQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPT 414
           |||||||||||||||||| |||||:||| |:|||| |:||||| ||:|||:||  ||||
Db    357  LEIIAFHCKSPNRHRMVVLEPLNKLLQEKWDRLVSRFFPNFACYLVYMFIFTVVAYHQPS 416

Qy    415  LKKQAAPHLKAEVGNSMLLTGHIILLLGTIYLVGQLWFWRRHVFIWISFDISYFEILF 474
           |:|| | |:|||:|:|||| |||:|:||  ||||||||| |:|||||:|||:|| |||
Db    417  LDQPAIPSSKATFGESMLLLGHILILLGGIYILLGQLWFWRRLFIWISFMDISYFEILF 476

Qy    475  LFQALLTVVSQVLCFIATEWYLPLLVSALVLGWLNLLYTRGFQHTGIYSVMIQKVILRD 534
           ||||||:|:||||| ||| ||||||:|||:||||||||| ||:|| || ||:|||:|||
Db    477  LLQALLTVLSQVLRFMETEWYLPLLVLSLVLGWLNLLYTRGDGTPDERWCVILRD 536

Qy    535  LIRFLLIYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGGQEDEGNGAQYRGIL 594
           :||:||||||:||||||:||||||| ||   |:: || |||  ||| | |||
Db    537  LLRFLLVYLIVFLFGFAVALVSLSREARSPKAPEDNNSTVTEQPTVGQEE--PAPYRSIL 594

Qy    595  EASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLITYILLLNMLILMSETVNSVAT 654
           :  ||||||||||||||||||||||| |:||||||||||||||||||||||| |||||
Db    595  DASLELFKFTIGMGELAFQEQLRFRGVVLLLLLAYVLLITYVLLLNMLIALMSETVNHVAD 654

Qy    655  DSWSIWKLQKAISVLEMENGYWWC-RKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNNAS 713
           :||||||||:|||||||||||||| |||||||||||||||||||||||||||||||:|
Db    655  NSWSIWKLQKAISVLEMENGYWWCRKKRKHREGRLLKVGTRGDGTPDERWCFRVEEVNNAA 714

Qy    714  WEQTLPTLCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQS 763
           ||:||||||||||||||||||||||||||||  :||||::|:|:|:|||
Db    715  WEKTLPTLSEDPSGPGITGNKKNPT----SKPGKNSASEEDHLPLQVLQS 760
```

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RESULT  6
ID    Q9JMI8           PRELIMINARY;         PRT;     762 AA.
AC    Q9JMI8;
DT    01-OCT-2000 (TrEMBLrel. 15, Created)
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT    01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE    ION CHANNEL.
OS    Rattus norvegicus (Rat).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX    NCBI_TaxID=10116;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Suzuki M.;
RC    TISSUE=KIDNEY;
RT    "Ion channel.";
RL    Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AB022322; BAA93435.1; -.
DR    InterPro; IPR002110; -.
DR    InterPro; IPR002111; -.
DR    Pfam; PF00023; ank; 3.
DR    PROSITE; PS50088; ANK_REPEAT; 1.
DR    PROSITE; PS50297; ANK_REP_REGION; 1.
SM    SMART; SM00248; ANK; 1.
SQ    SEQUENCE   762 AA;  86767 MW;  CE0970BC4195351E CRC64;
```

```
Query Match             75.6%;  Score 3028.5;  DB 11;  Length 762;
Best Local Similarity   77.4%;  Pred. No. 1.5e-230;
Matches  594;  Conservative  62;  Mismatches  94;  Indels  17;  Gaps  7;
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Qy      1  MTSPSPSSSPVFRLETLDGQOEDGSEADRGKLDFGSGLPPMESOFQGEDRKFAPQIRVNLNY 60
           |||:||| ||:| || | :|   :|||||| ||| ||||||:||:::||||| :|||||:
Db      1  MTSASSPPAFRLETSDGDEEGNAEVNKGKQE----PPPMESPFQREDRNSSPQIKVNLNF 56

Qy     61  ----RKGTGA-SOQPDNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGST 115
           |||| | || :|:|||:|||| ||:|:|||||:|||:||||||||||||||||||||||
Db     57  IKRPPKNTSAPSQOEPDRFDRDRLFSVVSRGVPEELTGLLEYLRWNSKYLTDSAYTEGST 116

Qy    116  GKTCLMKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGHSALHIAIEKRS 175
           |||||||||||||||||||||:||||||||||||||||||||||:|||||||||||||
Db    117  GKTCLMKAVLNLQODGVNACIMPLLQIDKDSGNPKLLVNAQCTDEFYQGHSALHIAIEKRS 176
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Qy  176  LQCVKLLVENGANVHARACGRFFQKGQGTCFYFGELPLSLAACTKQWDVVSYLLENPHQP  235
         |||||||||||| ||| |||||||| ||||||||||||||||||||||||||| ||||||
Db  177  LQCVKLLVENGADVHLRACGRFFQKHQGTCFYFGELPLSLAACTKQWDVVTYLLENPHQP  236

Qy  236  ASLQATDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDL  295
         ||| |||| |||||||||||| || ||  ||| ||||||||  |||||||||| | |  |
Db  237  ASLEATDSLGNTVLHALVMIADNSPENSALVIHMYDGLLQOMGARLCPTVQOLEEISNHQGL 296

Qy  296  TPLKLAAAKEGKIEIFRHILQOREFSG-LSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSV 354
         |||||||||||||||||||||||||||   |||||| |||||||||||||||| ||| ||||
Db  297  TPLKLAAAKEGKIEIFRHILQOREFSGYQPLSRKFJTEWCYGPVRVSLYDLSSVDSWEKNSV 356

Qy  355  LEIIAFHCKSPHRHRMVVLEPLNKLLQOAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPT  414
Db  356  ...

Qy  415  LKKQAAPHLKAEVGNSMLLTGHILLILLLGGIYLLLGGIYLLLGGQLWYFWRRHVFIWISF  416
Db  417  LDQPAIPSSKATFGESMLLGHIILLLLGGIYLLLGGQLWYFWRRHVFIWISFMDSYFEILF  476

Qy  417  LDQPAIPSSKATFGESMLLGHIILLLLGGIYLLLGGQLWYFWRRHVFIWISFMDSYFEILF
Db  477  LLQALLTVLSQVLRFMETENYLPLLVSLVLGWINLLYYTRGFQOHTGIYSYMIQOKVILRD  536

Qy  475  LFQALLTVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQOHTGIYSVMIQOKVILRD 534
Db  477  LLQALLTVLSQVLRFMETENYLPLLVSLVLGWINLLYYTRGFQOHTGIYSYMIQOKVILRD  536

Qy  535  LLRFLLIYLVFLFGFAVALVSLSQOEAWRPEAPTGPNATESVQPMEQCQEDEGNGAQYRGIL 594
Db  537  LLRFLIVYLVFLFGFAVALVSLSREARSKAPEDNNSTVTEQPTVGQEEE--PAPYRSIL    594

Qy  595  EASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAAVVLLTYILLLNMLIALMSETVNSVAT  654
Db  595  DASLELFKFTIGMGELAFQEQLRFRGVVLLLLLAAVVLLITYILLLNMLIALMSETVNHIVAD 654

Qy  595  DSWSWIKLQOKAISVLEMENGYWWC--RKKQORAGVMLTVGTKPDGSPEDERWCFRVEEVNWAS 713
Db  655  DSWSWIKLQOKAISVLEMENGYWWC--RKKQORAGVMLTVGTKPDGSPEDERWCFRVEEVNWAS 713

Qy  655  NSWSIWKLQKAISVLEMENGYWWCRRKKHREGRLLKVGTRGDGTPDERWCFRVEEVNWAA   714
Db  715  WEKTLPTLSEDPSGPGITGNKKNPT----SKPGKNSASEEDHLPLQV               757

Qy  714  WEQTLPTLCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQL                760
Db  715  WEKTLPTLSEDPSGPGITGNKKNPT----SKPGKNSASEEDHLPLQV               757
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RESULT 7

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ID   O35433      PRELIMINARY;      PRT;   838 AA.
AC   O35433;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR SUBTYPE 1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98007969; PubMed=9349813;
RA   Caterina M.J., Schumacher M.A., Tominaga M., Rosen T.A., Levine J.D.,
RA   Julius D.;
RT   "The capsaicin receptor: a heat-activated ion channel in the pain
RT   pathway.";
RL   Nature 389:816-824(1997).
DR   EMBL; AF029310; AAC53398.1; -.
DR   InterPro; IPR002110; -.
DR   InterPro; IPR002111; -.
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   SMART; SM00248; ANK; 1.
SQ   SEQUENCE   838 AA;   94947 MW;   DAFC80B12BDF71BF CRC64;
```

Query Match   41.3%;   Score 1652;   DB 11;   Length 838;
Best Local Similarity 46.3%;   Pred. No. 8e-122;

Matches 359;   Conservative 127;   Mismatches 230;   Indels 60;   Gaps 15;

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Qy   18  GQEDGSEADRGKLDFGSGLPPMESQFQGEDRRKFAPQIRVN---LNYRKGTG-------  65
Db   51  GKGDSEEAS----------PLDCPYEEGGLASCPIITVSSVLTIQRPGDGPASVRPSSQ  99

Qy   66  ----ASQPDNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSRKYLTDSEYTEGSTGKYCLM 121
Db  100  DSVSAGEKPPRLYDRRSIFDAVAQSNCQEELESLLPFLQRSKKRLTDSEFKDPETGKTCLL 159

Qy  122  KAVLNLKDGVNACILPLLQOIDRDSGNPEQPLVANAQCTDDYYRGHSALHIAIEKRSLQOCVKL 181
Db  160  KAMLNLHNGQNDTIALLLDVARKTDSLKQFVNASYTDSYYKGQTALHIAIERRNMTLVTL   219

Qy  182  LVENGANVHARACGRFFQKGQG-TCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA  240
Db  220  LVENGADVQAAANGDFFKKTKGRPGEYFGELPLSLAACTNQLAIVKRFLLQONSWQPADISA 279

Qy  241  TDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQODLTPLKL 300
Db  280  RDSVGNTVLHALVEVADNTVDNTKFVTSMYNEILILGAKLHPTLKLEEITNRKGLTPLAL  339

Qy  301  AAKEGKIEIFRHILQOREF--SGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEII 358
Db  340  AASSGKIGVLAYILQORIHEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVI  399

Qy  359  AF-HCKSPHRHRMVVLEPLNKLLQOAKWDLLIPK-FFLNFLCNLIYMFIFTAVAYHQPTLK 416
Db  400  AYSSSEFPNRHDMLLVEPLNRLLQODKNDRFVKRIFYFNFFVVCLYMIFTAAAYYRPV--  457

Qy  417  KQAAP--HLKAEVGNSMLLTGHILILLLGGIYLLLGGQLWYFWRRHVFIWISFIDSYFEILF 474
Db  458  -EGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFRGIQYFLQORRPSLKSLFVDSYSEILF  516

Qy  475  LFQALLITVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQOHTGIYSVMIQOKVILRD 534
Db  517  FVQSLFMLVSVVLYFSQORKEYVASMVFSLAMGWTNMLYYTRGFQOMGIYAVMIEKMILRD  576

Qy  535  LLRFLLIYLVFLFGFAVALVSLSQOEAWRPEAPTGPNATESVQPMEQCQEDEGNGA-----  588
Db  577  LCRFMFVYLVFLVFLGFSTAVVTLIED------GKN---NSLPMESTPHKCRGSACKPGN  625

Qy  589  QYRGILEASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAAVVLLLTYILLLNMLIALMSET 648
Db  626  SYNSLYSTCLELFKFTIGMGDLEFTENYDFKAVFIILLLAVVLTYILLLNMLIALMGET.   685

Qy  649  VNSVATDSWSWIKRLQOKAISVLEMENGYWWC--RKKQORAGVMLTVGTKPDGSPDERWCFRVE 707
Db  686  VNKIAQESKNIWKLQORAITILDTEKSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVD  745

Qy  708  EVNWASWEQTLPTLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQOLLQ      762
Db  746  EVNWTTWNTNVGIINEDPGNCEGVKRTLSFSLRSG----RVSGRMWKNFALVPLLR      797
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RESULT 8

```
ID   Q9JM57      PRELIMINARY;      PRT;   838 AA.
AC   Q9JM57;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR TYPE 1 LIKE PROTEIN 1.
GN   VRL1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tsutsumi S., Nakamura A., Kohama K.;
RT   "Vanilloid receptor type 1 like protein 1.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RESULT   9

ID    Q9H304
AC    Q9H304;
DT    01-MAR-2001 (TrEMBLrel. 16, Created)
DT    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT    01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE    CAPSAICIN RECEPTOR.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Cotright D.N., Peck A., Zou T.;
RL    "Cloning and characterization of the human capsaicin receptor, VR1.";
RL    Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RL    EMBL; AF196175; AAG43466.1; -.
KW    Receptor.
SQ    SEQUENCE   839 AA;  94968 MW;  EA9BF7D6O23EF9F4 CRC64;

Query Match             41.2%;  Score 1651.5;  DB 4;  Length 839;
Best Local Similarity   48.5%;  Pred. No. 8.8e-122;
Matches  344;  Conservative 122;  Mismatches 199;  Indels 45;  Gaps 11;

Qy       74 FDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNA 133
            :||:||| :|  :||  ||:|||||||:||||:|||||||||||||:||:||||||||||
Db      113 YDRRSIFEAVAQNNCQDLESLLFLQKSKKHLTDNEFKDPETGKTCLLRAMLNLHDGQNT 172

Qy      134 CILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHARA 193
            |||||||||||:||||||||||||||||||:||||||||:|::||:|||||||||||:|:
Db      173 TIPLLLEIARQTDSLKELVNASYDSYKGQTALHIAIERRNMALVTLLVENGADVQOAA 232

Qy      194 CGRFFQKQGQG-TCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTLVHAL 252
            ||| |||||| |||||||||||||||||:|||::||||:|||||||:|  ::|||||||
Db      233 HGDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTPADISARDSVGNTVLHAL 292

Qy      253 VMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
            ||::|||:|:|::|:|||:|||||||||||||||||||:||||||||::|
Db      293 VEVADNTADNTKFVTSMYNEILMLGAKLHPTLKLEELTNKKGMTPLALAAAGTGKIGVLAY 352

Qy      301 AAKEGKIEIFRHILQREF----SGLSHLSRKFTEWCYGPVRVSLIYDLASVDSCEENSVLEI 358
            :||||  ||  ||||:|:    |||||||||||||||||||||||:|||:|:|||||||||
Db      353 ILQREFS---GLSHLSRKFTEWCYGPVRVSLIYDLASVDSCEENSVLEIIAF-HCKSPHRIR 412

Qy      359 AF-HCKSPHRHRMVVLEPLNKLLQAKWDLLIPK--FFLNFLCNLIYMFIFTAVAYHQPTLK 416
            ||  |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db      413 MLIVEPLNRLLQDKWDREFVKRIFYFNFLVYCLYMIIFTMAAYYRPV---DGLPFKMEKI 469

Qy      417 KOAAP--HLKAEVGNSMLLTGHLILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILF 474
            |:|||  ||:| | :|||||||||||||||||||||||||||||||||:|||||||||||
Db      470 GDYFRVTGEILSVLGGVYFFFRGIQYFLQRRPSLKSLFVDSYSEILF 516

Qy      475 LFQALLTVVSQVLCFLAIEWYLPLLVSALVLGWLNLLIYTRGFQHTGIYSVMIQKVILRD 534
            ||||||||||| ||||:|||||||:||:||||||||||:|||||:||||||||||:||||
Db      517 CFLAIEWYLPLLVSALVLGWLNLLIYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLF 576

Qy      535 LLRFLLIYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGA---- 588
            ||:|||||||||||||||||||||||||||:||||||||||||||||||||||
Db      577 YFSHLKEVVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDCRFMEVYIVFLF 589

Qy      589 QYRGILEASLELFKFTIGMGELAFQEOLHFRGMVLLLLAYVLLTYILLLNMLIALMSET 648
            |:|||  |||||||||||:||||||:|||||||||||||||||:||||||||:||||||
Db      590 GFSPAVVTLIEDGKNDSLPSESTSHRWRGPACRPPDSS--------------- 632

Qy      649 VNSVATDSWSIWKLQRAISVLEMENGYWWC-RKKQRAGVMLTVGTKPDGSPDERWCFRVE 707
            |||||| ::||||||||||:|:||||||||||||:|:|| ||:||||||||||||||||||
Db      633 STCLELFKFTIGMGDLEFTENYDFKAVFIILLAYVILTYILLLNMLIALMGET 685

Qy      708 EVNWASWEQTLPTLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ 762
            :||| |:| |||||||:||::| ||||||||||||||||||||||||||||||||:
Db      686 VNKIAQESKNIKKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVD 745

Qy      746 EVNWTTWNTNVGIINEDPGNCEGVKRTLSFSLRSG----RVSGRNWKNFALVPLLR 797
            :|||:||||||||||||||||||||||||:||||:    ||||||||||||||:||
Db      746 EVNWASWEQTLPTLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ 762

Qy      714 WEQTLPTLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ 762
            |||||||||||||:| ||||||||||||||||||||||||||||||||||
Db      693 ESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGTTPDGKDDYRWCFRVDEVNWTT 752

Qy      753 WNTNVGIINEDPGNCEGVKRTLSFSLRSS----RVSGRNWKNFALVPLLR 798
            |||||||||||||||||||||||:|||||    |||||||||||||||||
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RESULT   10

ID    Q9H0G9
AC    Q9H0G9;
DT    01-MAR-2001 (TrEMBLrel. 16, Created)
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AC   Q9H0G9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   HYPOTHETICAL 94.9 KDA PROTEIN.
GN   DKFZP434K0220.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RA   Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL136801; CAB66735.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   839 AA;   94950 MW;  EA9BF7D603AE4760 CRC64;

Query Match             41.2%;  Score 1648.5;  DB 4;  Length 839;
Best Local Similarity   48.5%;  Pred. No.1.5e-121;
Matches  344;  Conservative  122;  Mismatches  199;  Indels  45;  Gaps  11;

Qy     74 FDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNA 133
          ::|| | ||||||||||||||||||:|||||||| ||||||||:||
Db    113 YDRRSIFEAVAQNNCQDLESLLFLQKSKKHLTDNEFKDPETGKTCLLKAMLNLHDGQNT 172

Qy    134 CILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHARA 193
          .| || | :| |  | || ||  |||:||| ::|| ||||:: :|| :|||||||:|:|
Db    173 TIPLLLETARQTDSLKELVNASYTDSYYKGQTALHIAIERRNMALVTLLVENGADVQAAA 232

Qy    194 CGRFFQKGQG-TCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHAL 252
          .| ||:   | ||||||||||||||:| | ||:|||:||::| |:|:|:|:|||||||||
Db    233 HGDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHAL 292

Qy    253 VMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAAKEGKIEIFRH 312
          | ::||:|:| ::||||:: :| |||| ||:::||| ||::  |||| ||  ||| ::
Db    293 VEVADNTADNTKFVTSMYNEILILGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAY 352

Qy    313 ILQREFS--GLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF-HCKSPHRHR 369
          |||||   | ||||||||||| |||| |||| ||   ||:|||||:|||: : |||
Db    353 ILQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHD 412

Qy    370 MVVLEPLNKLLQAKWDLLIPK-FFLNFLCNLIYMFIFTAVAVHQPTLKKQAAPHLKAE-V 427
          | :||||:|||:.||| : ||  |:|||||:|| |||||| |||| |:: : |  |||:|
Db    413 MLIVEPLNRLLQDKWDREVKRIFYFNFLVYCLYMIIFMAAYYRPV---DGLPPFKMEKI 469

Qy    428 GNSMLLTGHIILLLGGIYLLVGQLWFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVL 487
          |: :: |||| :| |||| ||| |:|:: |||:| |||||:|:|||||:|| ||||| |
Db    470 GDYFRVTGEILSVLGGVYFFFRGIQYFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVL 529

Qy    488 CFLAIEWYLPLLVSALVLGMLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLF 547
          .| : |   |::||:||:| : |||||||||: ||| |||:| ||||| ||: :::|||
Db    530 YFSHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVVIVFLF 589

Qy    548 GRAVALVSLSQEA---------WRPEAPIGPNATESVQPMEGQOEDEGNGANQYRGIL 594
          | ::|:| |  |          :        :  ||: |   |  : : |  ||
Db    590 GFSTAVVTLIEDGKNDSLPSESTSHRWRGPACRPPDSS------- 632

Qy    595 EASLELFKFTIGMGELAFQEQLHFRGMVLLLLAYVLLTYILLLNMLIALMSETVNSVAT 654
          : |||||||||||| |    : | |:|:|||||| ::|||| |||||||| ||||:::
Db    633 STCLELFKFTIGMGDLEFTENFDFKAVFILLLAYVILTYILLNMLIALMGETVNKIAQ 692

Qy    655 DSWSIWKLQKAISVLEMENGNYWWC-RKKORAGYWLTVGTKPDGSSPDERWCFRVEEVNNAS 713
          :| ||||||:||: : : |: ::   ||  | : :|:| |||| ::||:|||||::||: :
Db    693 ESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWTT 752

Qy    714 WEQTLPTLCEDPSGA--GVPRTLENPVLASPPKEDEDGASEENVYPVQLLQ 762
          | :   : ||| |    |  |||:   | |  : :  |        ||
Db    753 WNTNVGIINEDPQNCEGVKRTLSFSLRSS----RVSGRIWKNFALVPLLR 798
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RESULT 11
Q9NQ74
ID   Q9NQ74     PRELIMINARY;   PRT;   839 AA.
AC   Q9NQ74;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR 1.
GN   VR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hayes P., Meadows H.J., Harries M.H., Duckworth M.D., Cairns W.,
RA   Harrison D.C., Clarke C., Gunthorpe M., Ellington K., Prinjha R.K.,
RA   Barton A.J., Medhurst A.D., Smith G.D., Topp S., Murdock P.,
RA   Sanger G.J., Terrett J., Jenkins O., Randall A., Benham C.D.,
RA   Gloger I.S., Davis J.B.;
RT   "Cloning and functional expression of a human orthologue of rat
RT   vanilloid receptor-1.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RL   EMBL; AJ277028; CAB95729.1; -.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kelsell R.E.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   InterPro; IPR002110;
DR   InterPro; IPR002111;
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS00297; ANK; 1.
DR   SMART; SM00248; ANK; 1.
KW   Receptor.
SQ   SEQUENCE   839 AA;   94923 MW;  7142FFAE43189ECC CRC64;

Query Match             41.1%;  Score 1644.5;  DB 4;  Length 839;
Best Local Similarity   48.5%;  Pred. No. 3.1e-121;
Matches  344;  Conservative  121;  Mismatches  200;  Indels  45;  Gaps  11;

Qy     74 FDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNA 133
          ::|| | ||||||||||||||||||:|||||||| ||||||||:||
Db    113 YDRRSIFEAVAQNNCQDLESLLFLQKSKKHLTDNEFKDPETGKTCLLKAMLNLHDGQNT 172

Qy    134 CILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHARA 193
          .| || | :| |  | || ||  |||:||| ::|| ||||:: :|| :|||||||:|:|
Db    173 TIPLLLETARQTDSLKELVNASYTDSYYKGQTALHIAIERRNMALVTLLVENGADVQAAA 232

Qy    194 CGRFFQKGQG-TCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHAL 252
          .| ||:   | ||||||||||||||:| | ||:|||:||::| |:|:|:|:|||||||||
Db    233 HGDFFKKTKGRPGFYFGELPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHAL 292

Qy    253 VMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAAKEGKIEIFRH 312
          | ::||:|:| ::||||:: :| |||| ||:::||| ||::  |||| ||  ||| ::
Db    293 VEVADNTADNTKFVTSMYNEILILGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVLAY 352

Qy    313 ILQREFS--GLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF-HCKSPHRHR 369
          |||||   | ||||||||||| |||| |||| ||   ||:|||||:|||: : |||
Db    353 ILQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHD 412

Qy    370 MVVLEPLNKLLQAKWDLLIPK-FFLNFLCNLIYMFIFTAVAVHQPTLKKQAAPHLKAE-V 427
          | :||||:|||:.||| : ||  |:|||||:|| |||||| |||| |:: : |  |||:|
Db    413 MLIVEPLNRLLQDKWDREVKRIFYFNFLVYCLYMIIFMAAYYRPV---DGLPPFKMEKT 469

Qy    428 GNSMLLTGHIILLLGGIYLLVGQLWFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVL 487
          |: :: |||| :| |||| ||| |:|:: |||:| |||||:|:|||||:|| ||||| |
Db    470 GDYFRVTGEILSVLGGVYFFFRGIQYFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVL 529

Qy    488 CFLAIEWYLPLLVSALVLGMLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLF 547
          .| : |   |::||:||:| : |||||||||: ||| |||:| ||||| ||: :::|||
Db    530 YFSHLKEYVASMVFSLALGWTNMLYYTRGFQQMGIYAVMIEKMILRDLCRFMFVVVFLF 589
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RESULT 12
ID   Q9NY22        PRELIMINARY;   PRT;   839 AA.
AC   Q9NY22;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR 1.
GN   VR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=DORSAL ROOT GANGLION;
RA   McIntyre P., Winter J., Phillips E., Webb M., Chambers A.,
RA   Weerasekera N., Rang H., Savidge J., Clarke M., James I., Bevan S.,
RA   McLatchie L.;
RT   "Pharmacological comparison of human and rat VR1 expressed in CHO
RT   cells.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ272063; CAB89866.1; -.
DR   InterPro; IPR002110; -.
DR   InterPro; IPR002111; -.
DR   Pfam; PF00023; ank; 3.
DR   PROSITE; PS50088; ANK_REPEAT; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   SMART; SM00248; ANK; 1.
KW   Receptor.
SQ   SEQUENCE   839 AA;   94939 MW;   CC0D93A3AAD72F8 CRC64;

Query Match   40.9%;   Score 1636.5;   DB 4;   Length 839;
Best Local Similarity   48.2%;   Pred. No. 1.3e-120;
Matches 342;  Conservative 122;  Mismatches 201;  Indels 45;  Gaps 11;

Qy  548 GFAVALVSLSQEA-------------WRPEAPTGPNATESVQPMEGQOEDEGNGAQYRGIL 594
            ||: |:|:| :::                    || |||
Db  590 GFSTAVVTLIEDGKNDSLPSESTSHRWRGPACRPPDSS----------------YNSLY 632

Qy  595 EASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVAT 654
            |||||||||||| || : || ||| |||||||| || |: |||||||||| ||||| :
Db  633 STCLELFKFTIGMGDLEFTENYDFKAVFIILLLAYVILTIYILLLNMLIALMGETVNKIAQ 692

Qy  655 DSWSINKLQKAISVLEMENGYWWC-RKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWAS 713
            :|:||||||||| |: |   || ||| || ||||| ||| ||| :||| ||||||||| :
Db  693 ESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWTT 752

Qy  714 WEQTLPFLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ 762
            |  |   ||| ||    ||||| ||                  : ||
Db  753 WNTNVGIINEDPGNCEGVKRTLSFSLRSS-----RVSGRHWKNFALVPLLR 798
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RESULT 13
ID   Q9DFS3        PRELIMINARY;   PRT;   852 AA.
AC   Q9DFS3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL PROTEIN.
GN   VR-OAC.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COCHLEA;
RX   PubMed=11081638;
RA   Liedtke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,
RA   Hudspeth A.J., Friedman J.M., Heller S.;
RT   "Vanilloid Receptor-Related Osmotically Activated Channel (VR-OAC), a
RT   Candidate Vertebrate Osmoreceptor.";
RL   Cell 103:525-535(2000).
DR   EMBL; AF261883; AAG28026.1; -.
KW   Receptor.
SQ   SEQUENCE   852 AA;   96197 MW;   E85365D3FADD08C1 CRC64;

Query Match   36.6%;   Score 1467;   DB 13;   Length 852;
Best Local Similarity   41.7%;   Pred. No. 3.3e-107;
Matches 338;  Conservative 121;  Mismatches 245;  Indels 106;  Gaps 14;

Db  353 ILQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHD 412
Db  370 MVVLEPLNKLLQQAKWDLLLPK-FFLNFLCNLIYMFIFTAVAYHQPTLKKQAAPHLKAE-V 427
Db  413 MLLVEPLNRLLQDKWDRFVKRIFYFNELVYCLYMIIFTMAAYYRPV---DGLPPFKMEKT 469

Qy  428 GNSMLLTGHILILLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILLFLQALLTVVSGVL 487
Db  470 GDYFRVTGEILSVLGGVFFFRGIQYFLQKRPSMKTLFVDSYSEMLFFLQSLFMIATVVL 529

Qy  488 CFLAIEWYLPLLVSALVLGWLNLLLYYTRGFQHFGIYSVMIQKVILRDLLRFLLIYLVFLF 547
Db  530 YFSHLKEYVASMVFSLALGWTNMLYYTRGFQQOMGIYAVMIEKMILRDLCRFMFVYIVFLF 589

Qy  548 GFAVALVSLSQEA-------------WRPEAPTGPNATESVQPMEGQOEDEGNGAQYRGIL 594
Db  590 GFSTAVVTLIEDGKNDSLPSESTSHRWRGPACRPPDSS----------------YNSLY 632

Qy  595 EASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVAT 654
Db  633 STCLELFKFTIGMGDLEFTENYDFKAVFIILLLAYVILTIYILLLNMLIALMGETVNKIAQ 692

Qy  655 DSWSINKLQKAISVLEMENGYWWC-RKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWAS 713
Db  693 ESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWTT 752

Qy  714 WEQTLPFLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ 762
Db  753 WNTNVGIINEDPGNCEGVKRTLSFSLRSS-----RVSGRHWKNFALVPLLR 798
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Qy   74 FDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNA 133
Db  113 YDRSIFEAVAQNNCQDLESLLLFLQKSKKHLTDNEFKDPETGKTCLLKAMLNLHDGQNT 172

Qy  134 CILPLLQIDRDSGNPOPLVNAQCTDDYRGHSALHIAIEKRSLQCVKLLVENGANVHARA 193
Db  173 TIPLLLEIARQTDSLKELVNASYTDSYYKGQTALHIAIERNMALVTLLVENGADVQAAA 232

Qy  194 CGRFFQKGQG-TCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHAL 252
Db  233 HGDFFKKTKGRPGFYFGELPLSIAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHAL 292

Qy  253 VMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTIPLKLAAKEGKIEIFRH 312
Db  293 VEVADNTADNTFKFVTSMYNEILILGAKLHPTLKLEELTNKGMMPLALAAGTGKIGVLAY 352

Qy  313 ILQREFS---GLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF-HCKSPHRHR 369
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Qy   23 SEADRGKLDFGSGLPPMESQFQGEDRKFAPQIRVNL---------- 58
Db   37 AEPSRGRPPGAGDGKQNLRMKFHGAFRKGPPKPMELLESTIYESSSVVPAPKKAPMDSLFDY 96

Qy   59 -NYRK-------------------GTGASQPDP----NRFDRDRLFNAVSRGVPEDLAGLP 95
Db   97 GTYRQHPSENKRWRRRVVEKPVAGTKGPAPNPPPVLKVFNRPILFDIVSRGSPDGLEGLL 156

Qy   96 EYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNACILPLLQIDRDSGNPOPLVNAQ 155
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RESULT  14

ID   Q9HBC0          PRELIMINARY;     PRT;   871 AA.
AC   Q9HBC0;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   OTRPC4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   TISSUE=RENAL CORTEX;
RX   PubMed=11025659;
RA   Strotmann R., Harteneck C., Nunnenmacher K., Schultz G., Plant T.D.;
RT   "OTRPC4, a nonselective cation channel that confers sensitivity to
RT   extracellular osmolarity."
RL   Nat. Cell Biol. 2:695-702(2000).
DR   EMBL; AF258465; AAG16127.1; -.
SQ   SEQUENCE   871 AA;  98294 MW;  C62056B86DEA6FB6 CRC64;

Query Match             36.6%;    Score 1467;   DB 4;   Length 871;
Best Local Similarity   43.1%;
                        Pred. No. 3.4e-107;

Matches 339;   Conservative 114;   Mismatches 246;   Indels 88;   Gaps 16;
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Qy    157 SFLITHKKRLTDEEFEREPSTGKTCLPKALLNLSAGRNDTIPILLDIAEKTGNMREFINSP 216
          |||  :||||||                    ::||||||||||||:
Db    156 CTDDYYRGHSALHIAIEKRSLQCVKLLVVENGANVHARACGRFFQ-KGQGTCYFGELPLS 214

Qy    217 FRDVYYRGQTALHIAIERRCKHYVELLVELVEKGADVHAQAARGRFFQPKDEGGYFYFGELPLS 276
          :||:      ||||||:||||:|||||| ||||||||||:|||||
Db    215 LAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVMISDNSAENIALVTSMYDGLL 274

Qy    277 LAACTNQPHIVHYLTENGHKQADLRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLL 336
           ||| ||  :|   |   |  |:      |    ||||||||| :
Db    275 QAGARLCPTVQLEDIRNLQDLTPLKLAAKEGKIEIFRHILQREFS--GLSHLSRKFTEWC 332

Qy    337 IKCAKLFPDINLEALLNNDGLSPLMMAAKTGKIGIFQHIIRREIAEDVRHLSRKFKDWA 396
          |:||:|||||     |  |  |||  |||| |  |  ||| ||
Db    333 YGPVRVSLYDLASVDSC-EENSVLEIIAIFHCKSPHRHRMVVLEPLNKLLQAKWDLL-IPK 390

Qy    397 YGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVS 456
          |||: |||||| | |   :  |||||:||     |  ||:|||||:||  ||| |
Db    391 FFLNFLCNLIYMFIFTAVAVHQPTLKKQAAPHLKAEVGNSMLLTGHILLILGGIYLLVGQ 450

Qy    457 FYISVVSYLCAMIFTLIAYYRP--MEGPPYPYTTIYDYLRLAGEIITLITGILFFFSN 514
           :| | |: ||  | : :          :      ||:|  |  ||| |  |
Db    451 LW-YFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVLCFLAIENYLIPLLVSALVLGWLN 509

Qy    515 IKDLFMKKCPGVNSFPIDGSFQLLYFIYSVLVIVTAGLYLGGVEAYLAVAVFALVLGWMN 574
          |:||| |: |  | :|| ||| || : ||    |    | | |  || : |  | ||:
Db    510 LLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFAVALVSL-----SQE 559

Qy    575 ALYFTGLKILTGTYSIMIQKILFKDLFRFLLVYLLFMIGYASALVSLLNPCPSSESCCSED 634
          :|| ||: ||||| |||| |:|||| |  ||| | |  |  |  || :
Db    560 AWRPEAPTGPNATESVQPMEGQOEDEGNGAQYRGILEASLELFKFTIGMGELAFQEQLHFR 619

Qy    635 HSNCTLPTTYPSCRDS--------------QTFSTFLLDLFKLTIGMGDLEMLESAKYP 678
          |:|| |  ||||:|                     |||||  :
Db    635 HSNCTLPTTYPSCRDS--------------QTFSTFLLDLFKLTIGMGDLEMLESAKYP 678

Qy    679 GVFILLVTYIILTFVLLLNMLIALMGETVGQVSKESKHIWKLQWATTILDIERSFPLFL 738
          |: ::| || ||
Db    679 RKKQRAGVMLTVGIKPDGSPDERWCFRVEEVNWASWEQTLPTLCEDPSGAG-----729

Qy    739 RRAFRSGEMVTVGKGTDGTPDRRWCFRVDEVNWSHHNQNLGIISEDPGKSDTYQYYGFSH 798
          ||||||||||||| | |  ||||||||| |||::|:| ||
Db    730 --------------VPRTLENPVLASPPKED 746

Qy    799 TVGRLURDRWSTVVPRVE--LNKSCPTED 826
          |||| :||||||||:|
Db    799 TVGRLURDRWSTVVPRVE--LNKSCPTED 826
```

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RESULT  15

ID   Q9ER28          PRELIMINARY;     PRT;   871 AA.
AC   Q9ER28;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL.
GN   VROAC.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
```

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Qy      8 PVFRLETLDGGQEDG-----SEADRGK-LDFGSGGLPPMESQFQGEDRKFAP---------- 52
          |:||            ::|:        :::||:|  ||| ||
Db     32 PLSSLANLFEG-EDGSLSPSPADASRPAGPGDGRPNLRMKFQQAAFRKGVPNPIDLLESTL 90

Qy     53 ------------QIRVLNYRK-------------GTGASQPDP--NRFD 75
                           : ||                |||  ||
Db     91 YESSVVPGGKKAPMDSLFDYGTYRHHSSDNKRWRKKIIEKQPQSPKAPAPQPPPILKVFN 150

Qy     76 RDRLFNAVSRGYPEDLAGLPEYLSKTSKYLTDSEYTEGSSTGKTCLMKAVLNLKDGVNACI 135
          |:|| ||||  ||: |  | ||||::|||:
Db    151 RPILFDIVSRGSTPADLLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTI 210

Qy    136 LPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHARACG 195
          ||||    ||      |  ||:||||||||||||||||||||||||||||||||||||||
Db    211 PVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVELVEKGADVHAQARG 270

Qy    196 RFFQ-KGQGTCYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVM 254
          |||| |||||||||||||||||||||:||:|||||||||||||||| ||||||||||||
Db    271 RFFQPKDEGGYFYFGELPLSLAACTNQPHIVHYLTENPHKKADMRRQDSRGNTVLHALVA 330

Qy    255 ISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKKQAAPHLKAEVGNS 314
          |:||:|||||||||||||||||||||||||||||||||||||||| |:|:|| ||||
Db    331 IADNTRENTKFVTKMYDLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHII 390

Qy    315 QREFS--GLSHLSRKFTEWCYGPVRVSLYDLASVDSC-EENSVLEIIAIFHCKSPHRHRMV 371
           |:|   ||||||||||:|| | :||||||| | |     |||||:||
Db    391 RREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEAVLEILVYNSKIENRHEML 450

Qy    372 VLEPLNKLLQQAKWDLL-IPKFLNFLCNLIYMFIFTAVAVHQPTLKKQAAPHLKAEVGNS 430
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    451 AVEPINELLRDKWRKFQGAVSFYINVVSYLCAMVIFTLTAYYQPL--EGTPPYPYRTTVDY 508

Qy    431 MLLTGHILLILGGIYLLVGQLW-YFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVLCF 489
          |||||||||:|||||||||||| |||||||||||||||||||||||||||||||:| ||:
Db    509 LRLAGEVITLFCVLFPFTNIKDLFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVTAGLYL 568

Qy    490 LAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGF 549
          |||  |||:| ||||||||| | |||||||||||||||||||||||||||||||||||||
Db    569 AGIEAYLAVAVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY 628

Qy    550 AVALVSL--------SQEAWRPEAPTGPNATESVQPMEGQOEDEGNGAQYRGILEASLE 599
          |||||||        ||||||||||||||||||||||||||||||||||||||||||||
Db    629 ASALVSLLNPCANMKVCNEDQTNCTVPTYPSCRDS-----ETFSTFL--LD 672

Qy    600 LFKFTIGMGELAFQEQLHFRGMVLLLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSI 659
          |||||||||||||||||||||||:::|  ||||||||||||||||||||||||:||||||||
Db    673 LFKLTIGMGDLEMLSSTRKYPVVFIILLVTYILLTFVLLLNMLIALMGETVGQVSKESKHI 732

Qy    660 WKLQKAISVLEMENGY-WWCKRKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTL 718
          ||||  ||||||:| | ||||: |:||||||| |||||||||||||||| |||||:|| |
Db    733 WLQWATTILDIERSFPVFLRKAFRSGEMVTVGKSSDGTPDRRWCFRVDEVNWSHWNQNL 792

Qy    719 PTLCEDP 725
          ||||||
Db    793 GIINEDP 799
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RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   PubMed=11081638;
RA   Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA   Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT   "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT   candidate vertebrate osmoreceptor.";
RL   Cell 103:525-535(2000).
DR   EMBL; AF263521; AAG28027.1; -.
KW   Receptor.
SQ   SEQUENCE    871 AA;   98009 MW;   5D50684DA08C354B CRC64;

Qy             757 PVQLL 761
                   |:| |
Db             844 PLDNL 848

Search completed: July 18, 2001, 16:00:08
Job time: 136 sec

Query Match             36.6%;  Score 1465.5;  DB 11;  Length 871;
Best Local Similarity   40.4%;  Pred. No. 4.5e-107;
Matches  341;  Conservative 128;  Mismatches 257;  Indels 119;  Gaps  16;

Qy      8 PVFRLETHLDGGQOEDGS------------EADRGKLDFGSGLPPMESQFQGEDRKFAP---------- 52
          :|  |    |   | |  |           :|:|
Db     32 PLSSLANLFEGEEGSSSLSPVDASR-PAGPGDGRPNLRMKFQGAFRKGVPNPIDLLESTL 90

Qy     53 -------------QIRVNLNYRKGTGASQPDPNR-------------------- ---FD 75
                       |   |                                       |:
Db     91 YESSVVPGPKKAPMDSLFDYGTYRHHPSDNKRWRKVVEKQPQSPRAPAPQPPPILKVFN 150

Qy     76 RDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNACI 135
          ||||  |  |  | |  | |  || | | || |||   | | | | |  | |:||| | |
Db    151 RPILFDIVSRGSTADLDGLLSYLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTI 210

Qy    136 LPLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVKLLVENGANVHARACG 195
          | | |  ||| |  |  |  |  | | ||:|| |:|| || | |||||| ||| |:| |
Db    211 PVLLDIAERTGNMREFINSPFRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARG 270

Qy    196 RFFQ-KGQGTCYFGGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVM 254
          ||||    ||| | |||| || ||| |  |:||||||| |    | | | ||||||||| 
Db    271 RFFQPKDEGGYFYFGGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVA 330

Qy    255 ISDNSAENIALVTSMYDGLLQQAGARLCPTVQLEDIRNLQDLTPLKLAAAKEGKIEIFRHIL 314
          |::| ||| ||  |  ||::||||| | ||| ||:|||  | | ||  | |  | |||| | 
Db    331 IADNTRENTKFVTKMYIDLLLKCSRLFPDSNLETVLNNDGLSPLMAAKTGKIGVFQHII 390

Qy    315 QREFS--GLSHLSRKFTEWCYGPVRVSLYDLASVDSC-EENSVLEIIAFHCKSPHRHRMV 371
          ||     |: |:||    | |||| |:|| | :|| |  | | | | | |:  | | |||
Db    391 RREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML 450

Qy    372 VLEPLNKLLQAKWDLL--IPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQOAAPHLKAEVGNS 430
          ::|:|:| |      |  | |:| | | ||| ||| | ||| ||:  |  | || |  |||
Db    451 AVEPINELLRDKWRKFGAVSPYINVVSYLCAMVIFLTAYYQPL--EGTPYPYRTTVDY 508

Qy    431 MLLTGHILILLGGIYLLVGQLM--YFWRHVFIWISFIDSYFEILFLFQOALLTVVSQVLCF 489
          | | | | :| | ||||||| |  | |  |||  || | |  | |   | ||| || | |:
Db    509 LRLAGEVITLLITGVLFFTSIKDLFMKKCPGVNSLFVDGSFQLLYFIYSVLVVVSAALYL 568

Qy    490 LAIEWYLPLIVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGF 549
          | | | ||  |  || ||:| :||:||  |||| ||| | |:|:  | | | | |  |
Db    569 AGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLLVYLLFMIGY 628

Qy    550 AVALVSL----------SQEAWRPEAPTGPNATESVQPMEGGQEDEGNGAQYRGILEASLE 599
           :|| :|          :  | | |  ||                        |:| |  
Db    629 ASALVTLLNPCTNMKVCNEDQSNCTVPSYPACRDS-------------------ETFSAFL---LD 672

Qy    600 LFKFTIGMGELAFQEQLHFRGMVLLLLLLAYVLLTYILLLNMLIALMSETVNSVATDSWSI 659
          ||||| ||| | | || | | |:| | | | |||| |||| ||||||| | || | |:|:
Db    673 LFKLTIGMGDLEMLSSAKYPVVFILLLVTYILLTFVLLLNMLIALMGETVGQVSKESKHI 732

Qy    660 WKLQKAISVLEMENGY-WWCRKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTL 718
          ||||   | :  ||:| | ||||   | : | |  | |  |  ||  |  || |  ||:|
Db    733 WKLQWATTILDIERSFPVFLRKAFRSGEMVTVGKSSDGTPDRRWCFRVDEVNWSHWNQNL 792

Qy    719 PTLCEDPS--------------------GAGVPRTLENVLASPRKEDEDGASEENYV 756
                                       ||| |  |::  |:  || |::| ||
Db    793 GIINEDPGKSEIYQYGFSHIMGRLRRDRWSSVVPRVVE--------LNKNSGTDEVVV 843
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